

CRFI #32



1600

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/347,064F

DATE: 05/13/2003

TIME: 09:10:14

Input Set : N:\efs\09347064\SL7.txt

Output Set: N:\CRF4\05122003\I347064F.raw

TECH CENTER 1600/2900

MAY 15 2003

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3 <110> APPLICANT: Eck, Jorgen
4      Schmidt, Arno
5      Zinke, Holger
7 <120> TITLE OF INVENTION: Recombinant Fusion Proteins Based on
8      Ribosome-Inactivating Proteins of the mistletoe Viscum
9      album
11 <130> FILE REFERENCE: 09282-5
13 <140> CURRENT APPLICATION NUMBER: 09/347,064F
14 <141> CURRENT FILING DATE: 1999-07-02
16 <150> PRIOR APPLICATION NUMBER: PCT/EP98/00009
17 <151> PRIOR FILING DATE: 1998-01-02
19 <150> PRIOR APPLICATION NUMBER: EP 97 10 0012.0
20 <151> PRIOR FILING DATE: 1997-01-02
22 <160> NUMBER OF SEQ ID NOS: 38
24 <170> SOFTWARE: PatentIn Ver. 2.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 762
28 <212> TYPE: DNA
29 <213> ORGANISM: Viscum album
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33 cggttcatca cgcttctccg agattatgtc tcaagcggaa gcttttccaa tgagatacca 120
34 ctcttgcgtc agtctacgat ccccgctctcc gatgcgcgaaa gatttgtctt ggtggagctc 180
35 accaaccagg ggggagactc gatcacggcc gccatcgacg ttaccaatct gtacgtcgtg 240
36 gcttaccgag caggcgacca atcctacttt ttgcgcgacg caccacgcgg cgcggaaacg 300
37 catctcttca ccggcaccac ccgatacctc ctcccattca acggaagcta ccctgatctg 360
38 gagcgatacg ccggacatag ggaccagatc cctctcggtg tagaccaact cattcaatcc 420
39 gtcacggcgc ttcgttttcc gggcggcagc acgcgtaccc aagctcgttc gattttaatc 480
40 ctcatcaga tgatctccga ggccgccaga ttcaatccca tcttatggag ggctcgccaa 540
41 tacattaaca gtggggcgtc atttctgcca gacgtgtaca tgctggagct ggagacgagt 600
42 tggggccaac aatccacgca agtccagcat tcaaccgatg gcgtttttaa taaccaatt 660
43 cggttggcta taccgcccgg taacttcgtg acgttgacca atgttcgcga cgtgatcgcc 720
44 agcttgccga tcatgttggt tgtatgcgga gagcgcgccg gt 762
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48 <211> LENGTH: 252
49 <212> TYPE: PRT
50 <213> ORGANISM: Viscum album
52 <400> SEQUENCE: 2
53 Met Tyr Glu Arg Ile Arg Leu Arg Val Thr His Gln Thr Thr Gly Glu
54 1 5 10 15
56 Glu Tyr Phe Arg Phe Ile Thr Leu Leu Arg Asp Tyr Val Ser Ser Gly
57 20 25 30
59 Ser Phe Ser Asn Glu Ile Pro Leu Arg Gln Ser Thr Ile Pro Val

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60          35          40          45
62 Ser Asp Ala Gln Arg Phe Val Leu Val Glu Leu Thr Asn Gln Gly Gly
63          50          55          60
65 Asp Ser Ile Thr Ala Ala Ile Asp Val Thr Asn Leu Tyr Val Val Ala
66 65          70          75          80
68 Tyr Gln Ala Gly Asp Gln Ser Tyr Phe Leu Arg Asp Ala Pro Arg Gly
69          85          90          95
71 Ala Glu Thr His Leu Phe Thr Gly Thr Thr Arg Ser Ser Leu Pro Phe
72          100          105          110
74 Asn Gly Ser Tyr Pro Asp Leu Glu Arg Tyr Ala Gly His Arg Asp Gln
75          115          120          125
77 Ile Pro Leu Gly Ile Asp Gln Leu Ile Gln Ser Val Thr Ala Leu Arg
78          130          135          140
80 Phe Pro Gly Gly Ser Thr Arg Thr Gln Ala Arg Ser Ile Leu Ile Leu
81 145          150          155          160
83 Ile Gln Met Ile Ser Glu Ala Ala Arg Phe Asn Pro Ile Leu Trp Arg
84          165          170          175
86 Ala Arg Gln Tyr Ile Asn Ser Gly Ala Ser Phe Leu Pro Asp Val Tyr
87          180          185          190
89 Met Leu Glu Leu Glu Thr Ser Trp Gly Gln Gln Ser Thr Gln Val Gln
90          195          200          205
92 His Ser Thr Asp Gly Val Phe Asn Asn Pro Ile Arg Leu Ala Ile Pro
93          210          215          220
95 Pro Gly Asn Phe Val Thr Leu Thr Asn Val Arg Asp Val Ile Ala Ser
96 225          230          235          240
98 Leu Ala Ile Met Leu Phe Val Cys Gly Glu Arg Pro
99          245          250
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103 <211> LENGTH: 828
104 <212> TYPE: DNA
105 <213> ORGANISM: Viscum album
107 <400> SEQUENCE: 3
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110 cagttgtggc cctccaagtc caacaatgat ccgaatcagt tgtggacgat caaaagggat 180
111 ggaaccattc gatccaatgg cagctgcttg accacgtatg gctatactgc tggcgtctat 240
112 gtgatgatct tcgactgtaa tactgctgtg cgggaggcca ctctttggca gatatggggc 300
113 aatgggacca tcatcaatcc aagatccaat ctggttttgg cagcatcatc tggaatcaaa 360
114 ggcactacgc ttacgggtgca aacactggat tacacgttgg gacagggctg gcttgccggc 420
115 aatgataccg cccacgcgca ggtgaccata tatgggttca gggaccttg catggaatca 480
116 aatggaggga gtgtgtgggt ggagacgtgc gtgagtagcc aaaagaacca aagatgggct 540
117 ttgtacggg atggttctat acgccccaaa caaaaccaag accaatgcct cacctgtggg 600
118 agagactccg tttcaacagt aatcaatata gttagctgca gcgctggatc gtctgggcag 660
119 cgatgggtgt ttaccaatga aggggccatt ttgaatttaa agaatgggtt ggccatggat 720
120 gtggcgcaag caaatccaaa gtcgcgccga ataatcatct atcctgccac aggaaaacca 780
121 aatcaaatgt ggcttcccgt gccaggtgga tatcactagt aaggatcc 828
124 <210> SEQ ID NO: 4
125 <211> LENGTH: 267
126 <212> TYPE: PRT

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133 Arg Asn Gly Met Cys Val Asp Val Arg Asp Asp Phe Arg Asp Gly
134   20          25          30
136 Asn Gln Ile Gln Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln
137   35          40          45
139 Leu Trp Thr Ile Lys Arg Asp Gly Thr Ile Arg Ser Asn Gly Ser Cys
140   50          55          60
142 Leu Thr Thr Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp
143  65          70          75          80
145 Cys Asn Thr Ala Val Arg Glu Ala Thr Leu Trp Gln Ile Trp Gly Asn
146   85          90          95
148 Gly Thr Ile Ile Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser
149  100         105         110
151 Gly Ile Lys Gly Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu
152  115         120         125
154 Gly Gln Gly Trp Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr
155  130         135         140
157 Ile Tyr Gly Phe Arg Asp Leu Cys Met Glu Ser Asn Gly Gly Ser Val
158 145         150         155         160
160 Trp Val Glu Thr Cys Val Ser Ser Gln Lys Asn Gln Arg Trp Ala Leu
161 165         170         175
163 Tyr Gly Asp Gly Ser Ile Arg Pro Lys Gln Asn Gln Asp Gln Cys Leu
164 180         185         190
166 Thr Cys Gly Arg Asp Ser Val Ser Thr Val Ile Asn Ile Val Ser Cys
167 195         200         205
169 Ser Ala Gly Ser Ser Gly Gln Arg Trp Val Phe Thr Asn Glu Gly Ala
170 210         215         220
172 Ile Leu Asn Leu Lys Asn Gly Leu Ala Met Asp Val Ala Gln Ala Asn
173 225         230         235         240
175 Pro Lys Leu Arg Arg Ile Ile Tyr Pro Ala Thr Gly Lys Pro Asn
176 245         250         255
178 Gln Met Trp Leu Pro Val Pro Gly Gly Tyr His
179 260         265
182 <210> SEQ ID NO: 5
183 <211> LENGTH: 72
184 <212> TYPE: DNA
185 <213> ORGANISM: Viscum album
187 <400> SEQUENCE: 5
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189 gatgttacat gt 72
192 <210> SEQ ID NO: 6
193 <211> LENGTH: 17
194 <212> TYPE: PRT
195 <213> ORGANISM: Viscum album
197 <400> SEQUENCE: 6
198 Ser Ser Ser Glu Val Arg Tyr Trp Pro Leu Val Ile Arg Pro Val Ile

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200 Ala
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205 <213> ORGANISM: Viscum album
207 <400> SEQUENCE: 7
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209 atcacgcttc tccgagatta tgtctcaagc ggaagctttt ccaatgagat accactcttg 120
210 cgtcagtcta cgatccccgt ctccgatgcg caaagatttg tcttggtgga gctcaccaac 180
211 caggggggag actcgatcac ggccgccatc gacgttacca atctgtacgt cgtggcttac 240
212 caagcaggcg accaatccta ctttttgccg gacgcaccac gcggcgcgga aacgcatctc 300
213 ttcaccggca ccaccgatc ctctctccca ttcaacggaa gctaccctga tctggagcga 360
214 tacgccggac atagggacca gatccctctc ggtatagacc aactcattca atccgtcacg 420
215 gcgcttcggt ttcggggcgg cagcacgcgt acccaagctc gttcgatttt aatcctcatt 480
216 cagatgatct ccgaggccgc cagattcaat cccatcttat ggagggtctg ccaatacatt 540
217 aacagtgggg cgtcatttct gccagacgtg tacatgctgg agctggagac gagttggggc 600
218 caacaatcca cgcaagtcca gcattcaacc gatggcggtt ttaataaccc aattcgggtg 660
219 gctatacccc ccggttaactt cgtgacgttg accaatgttc gcgacgtgat cgccagcttg 720
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225 <212> TYPE: PRT
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228 <400> SEQUENCE: 8
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232 Tyr Phe Arg Phe Ile Thr Leu Leu Arg Asp Tyr Val Ser Ser Gly Ser
233      20              25              30
235 Phe Ser Asn Glu Ile Pro Leu Leu Arg Gln Ser Thr Ile Pro Val Ser
236      35              40              45
238 Asp Ala Gln Arg Phe Val Leu Val Glu Leu Thr Asn Gln Gly Gly Asp
239      50              55              60
241 Ser Ile Thr Ala Ala Ile Asp Val Thr Asn Leu Tyr Val Val Ala Tyr
242      65              70              75              80
244 Gln Ala Gly Asp Gln Ser Tyr Phe Leu Arg Asp Ala Pro Arg Gly Ala
245      85              90              95
247 Glu Thr His Leu Phe Thr Gly Thr Thr Arg Ser Ser Leu Pro Phe Asn
248      100             105             110
250 Gly Ser Tyr Pro Asp Leu Glu Arg Tyr Ala Gly His Arg Asp Gln Ile
251      115             120             125
253 Pro Leu Gly Ile Asp Gln Leu Ile Gln Ser Val Thr Ala Leu Arg Phe
254      130             135             140
256 Pro Gly Gly Ser Thr Arg Thr Gln Ala Arg Ser Ile Leu Ile Leu Ile
257      145             150             155             160
259 Gln Met Ile Ser Glu Ala Ala Arg Phe Asn Pro Ile Leu Trp Arg Ala
260      165             170             175
262 Arg Gln Tyr Ile Asn Ser Gly Ala Ser Phe Leu Pro Asp Val Tyr Met
263      180             185             190

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265 Leu Glu Leu Glu Thr Ser Trp Gly Gln Gln Ser Thr Gln Val Gln His
266      195      200      205
268 Ser Thr Asp Gly Val Phe Asn Asn Pro Ile Arg Leu Ala Ile Pro Pro
269      210      215      220
271 Gly Asn Phe Val Thr Leu Thr Asn Val Arg Asp Val Ile Ala Ser Leu
272 225      230      235      240
274 Ala Ile Met Leu Phe Val Cys Gly Glu Arg Pro Ser
275      245      250
278 <210> SEQ ID NO: 9
279 <211> LENGTH: 789
280 <212> TYPE: DNA
281 <213> ORGANISM: Viscum album
283 <400> SEQUENCE: 9
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285 tgcgtggacg tccgagatga cgatttcgcg gatggaaatc agatacagtt gtggccctcc 120
286 aagtccaaca atgatccgaa tcagttgtgg acgatcaaaa gggatggaac cattcgatcc 180
287 aatggcagct gcttgaccac gtatggctat actgctggcg tctatgtgat gatcttcgac 240
288 tgtaatactg ctgtgcggga ggccactctt tggcagatat ggggcaatgg gaccatcatc 300
289 aatccaagat ccaatctggt tttggcagca tcactctggaa tcaaaggcac tacgcttacg 360
290 gtgcaaacac tggattacac gttgggacag ggctggcttg ccggtaatga taccgcccc 420
291 cgcgaggtga ccatatatgg gttcagggac ctttgcatgg aatcaaattg agggagtgtg 480
292 tgggtggaga cgtgcgtgag tagccaaaag aaccaaatga gggctttgta cggggatggt 540
293 tctatacgcc ccaaacaaaa ccaagaccaa tgccctacct gtgggagaga ctccgtttca 600
294 acagtaatca atatagttag ctgcagcgct ggatcgtctg ggcagcgatg ggtgtttacc 660
295 aatgaagggg ccattttgaa tttaaagaat gggttggcca tggatgtggc gcaagcaa 720
296 ccaaagctcc gccgaataat catctatcct gccacaggaa aaccaaatac aatgtggctt 780
297 cccgtgcca 789
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301 <211> LENGTH: 263
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310      20      25      30
312 Asn Gln Ile Gln Leu Trp Pro Ser Lys Ser Asn Asn Asp Pro Asn Gln
313      35      40      45
315 Leu Trp Thr Ile Lys Arg Asp Gly Thr Ile Arg Ser Asn Gly Ser Cys
316      50      55      60
318 Leu Thr Thr Tyr Gly Tyr Thr Ala Gly Val Tyr Val Met Ile Phe Asp
319 65      70      75      80
321 Cys Asn Thr Ala Val Arg Glu Ala Thr Leu Trp Gln Ile Trp Gly Asn
322      85      90      95
324 Gly Thr Ile Ile Asn Pro Arg Ser Asn Leu Val Leu Ala Ala Ser Ser
325      100      105      110
327 Gly Ile Lys Gly Thr Thr Leu Thr Val Gln Thr Leu Asp Tyr Thr Leu
328      115      120      125
330 Gly Gln Gly Trp Leu Ala Gly Asn Asp Thr Ala Pro Arg Glu Val Thr

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**VERIFICATION SUMMARY**

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